

## FIGURE 108

GCCTGCCGTTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCTGCAC  
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCCGCCCTGCCCGG  
ACCGGTCGCCCGCTTTTGTGTAACCTTAAAGCGGGCGCAGCATTAAGCTTCCGCCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG  
CAGGTCTGAGCCTCGAGCCGAGCAGCAGCTCAAATTCGAGGTCCCTTCCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTTGTTTAAAGTTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAGGGGCTCAATT  
AATGATTCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTCAGTCTATGTTTGCTCCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTTGTTTGAATTGCCAGCAGAGAAAT  
GATAAACCCACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAGGTGAAGTTTCAAGGCTACGGGAGGAGAACAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTGTCTTTA  
TCGTTGGTGTAAATTATTGGGAAGATTGCCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTATCATAACCATGTGTAAGAAAGAAATT  
AATGTATGATGACATCTCAGAGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACAAAATATAATGTAAACGATCTTTAGAAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAAATGACAAGGGAAACCATGAGTAATGCCAAT  
GGCATATTGTAATGTCATTTTAAACATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT  
GCTGGGGAGTGCGGTTCAGCTCCACACAGTAGTCCCACGTGGCCCACTCCCGCCAGGCTG  
CTTCCGTGTCCTTCAAGTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
GCTAAATTTGATTGTTTATGATGATGAAAGTCAAACCTGTTATTAGAGATGTTTAAATGCATA  
TTTAACTTATTAAATGATTTTATCTCATGTTTTCTTATTGTCAACAAGATACAGTTAATGC  
TGCGTGCTGCTGAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTGTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAAACTCTTCAGCGAATCCTCTAGTAGC  
TAGTTGAGAGTTTGAAGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAGAAAAATTTATAATAAGCCCCAAAATTAAGAAAA

09978295.101501

## FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHCLKFRGPF<sup>1</sup>TDVVTTNLKLG<sup>2</sup>NPTDRNVC<sup>3</sup>FKVKT<sup>4</sup>TAPRRYCVRPNSGIID  
AGASINVSVM<sup>5</sup>LQPF<sup>6</sup>YDPNEKSKHKFMVQSMF<sup>7</sup>APT<sup>8</sup>DTSDMEAVWKEAKPEDLMDSKLRCVFE  
LPAENDKPHDVEINKIIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLMRMRTVQSN<sup>9</sup>SPISALAPT<sup>10</sup>GKEEGLSTRLLALVVLFFIVGVII<sup>11</sup>GKIAL

### **Important features:**

#### **Transmembrane domain:**

amino acids 224-239

#### **N-glycosylation site.**

amino acids 68-71

#### **N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

[illegible]

GTCACTCTTCTAGATGTCTTATCCCACTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAGACNAACCCAGTTCGTGTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCC  
CAAATAATTAGAAATTCCTTTGTCAATTTGTCACTTTGTCAATTTGCTATGGGGGGAATTATTATTTT  
ATCATTTTTTATTATTTTGCCATTGGGAAGGTAACTTTAAATAGAC